

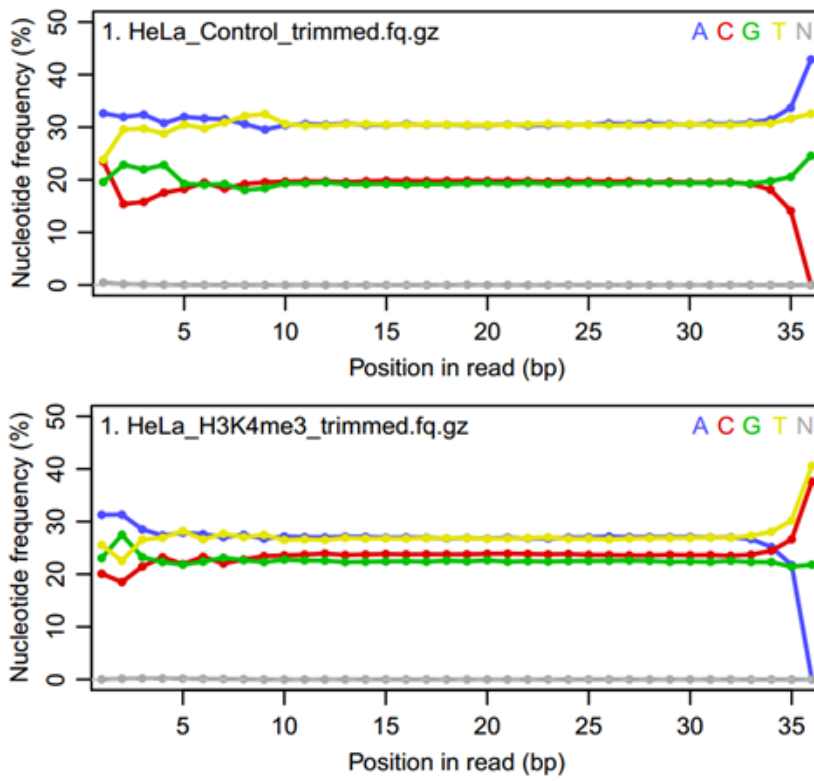
## **SUPPLEMENTARY INFORMATION**

### **A ChIP-Seq Data Analysis Pipeline Based on Bioconductor Packages**

**Seung-Jin Park<sup>1,2</sup>, Jong-Hwan Kim<sup>1,2</sup>, Byung-Ha Yoon<sup>1,2</sup>, Seon-Young Kim<sup>1,2\*</sup>**

<sup>1</sup>Personalized Genomic Medicine Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon 34141, Korea,

<sup>2</sup>Department of Functional Genomics, University of Science and Technology (UST), Daejeon 34113, Korea



**Supplementary Fig. 1.** Nucleotide frequency. These plots show the frequency of A, C, G, T, and N bases by position in the input reads.